Reactivation of HIV-1 proviruses in immune-compromised mice engrafted with human VOA-negative CD4+ T cells

Zhe Yuan  
*University of Nebraska-Lincoln*, s-zyuan1@unl.edu

Guobin Kang  
*University of Nebraska–Lincoln*, gkang2@unl.edu

Wuxun Lu  
*University of Nebraska - Lincoln*

Qingsheng Li  
*University of Nebraska-Lincoln*, qli4@unl.edu

Follow this and additional works at: https://digitalcommons.unl.edu/virologypub

Part of the Biological Phenomena, Cell Phenomena, and Immunity Commons, Cell and Developmental Biology Commons, Genetics and Genomics Commons, Infectious Disease Commons, Medical Immunology Commons, Medical Pathology Commons, and the Virology Commons

Yuan, Zhe; Kang, Guobin; Lu, Wuxun; and Li, Qingsheng. "Reactivation of HIV-1 proviruses in immune-compromised mice engrafted with human VOA-negative CD4+ T cells" (2017). *Virology Papers*. 361.  
https://digitalcommons.unl.edu/virologypub/361

This Article is brought to you for free and open access by the Virology, Nebraska Center for at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Virology Papers by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.
Reactivation of HIV-1 proviruses in immune-compromised mice engrafted with human VOA-negative CD4+ T cells

Zhe Yuan, Guobin Kang, Wuxun Lu and Qingsheng Li*

Nebaska Center for Virology, School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA

Abstract

**Background:** HIV-1 infection remains incurable on antiretroviral therapy (ART); however, HIV-1 infection remains incurable due to virus latency [1–3]. To better understand the mechanisms of HIV-1 latency and develop strategies to purge latent infection, quantitative in vitro assays and in vivo animal models to study HIV-1 latency and evaluate latency-reversing agents (LRAs) are critically needed. However, VOA can only reactivate a small fraction of intact proviruses.

**Methods:** To explore the utility of NOD scid gamma (NSG) mice as an in vivo model to reactivate HIV-1 proviruses from VOA-negative CD4+ T cells, resting CD4+ T cells from an HIV-1 latently infected individual were isolated and the human CD4+ T cells corresponding to VOA-positive and VOA-negative CD4+ T cells were engrafted into NSG mice. Plasma viral load (pVL) and human CD4+ T cells were quantified every other week using qRT-PCR and flow cytometry.

**Results:** We found that NSG mice reactivated latently infected HIV-1 from VOA-positive CD4+ T cells as well as VOA-negative CD4+ T cells. Engrafted CD4+ T cells proliferated considerably in vivo, peaked prior to provirus reactivation, and lasted for up to 14 weeks. Sequence analyses revealed that reactivated proviruses in VOA-positive and VOA-negative CD4+ T cells are different.

**Conclusion:** Taken together, NSG mice can support long-term engraftment of human CD4+ T cells and reactivate VOA-positive and VOA-negative proviruses. Therefore, this in vivo model has the potential to be used to study the underlying mechanisms of HIV-1 latency and reactivation.

Keywords: HIV-1 latency, viral outgrowth assay, immune-compromised mice, in vivo provirus reactivation, resting CD4+ T cells, clonal expansion

Introduction

Remarkable progress has been made in reducing the mortality and morbidity of HIV-1 infection through combined antiretroviral therapy (ART); however, HIV-1 infection remains incurable due to virus latency [1–3]. To better understand the mechanisms of HIV-1 latency and develop strategies to purge latent infection, quantitative in vitro assays and in vivo animal models to study HIV-1 latency and evaluate latency-reversing agents (LRAs) are critically needed. As such, major quantitative assays, namely inverse PCR [4,5], improved Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs. Enhanced co-culture assays, including Alu PCR [6–8] and linker-primer PCR [9], have been previously developed. Although these methods can quantify the frequency of proviruses, they cannot distinguish between defective and functional/intact proviruses, thus often overestimating the size of the latent reservoirs.
Methods

Study subject

PBMCs were obtained from an HIV-1 infected individual, who had 14.3 years of diagnosed infection and continuous suppression of plasma HIV-1 with ART (emtricitabine-tenofovir, ritonavir and atazanavir) at undetectable levels (<50 copies/mL) for 6.3 years prior to sampling time. The CD4 cell count was 627 cells/µm³ at the time of this study. The infected donor exhibited 0.518 infectious units per million (IUPM). This study was approved by the Johns Hopkins Institutional Review Board, written informed consent was obtained from all participants as per a previous report [10].

Human resting CD4+ T cell isolation and virus outgrowth assay

Resting CD4+ T cells were isolated from the PBMCs of the HIV-1+ donor by negative selection using the CD4+ T Isolation Kit II with CD25, CD69 and HLA-DR microbeads (Miltenyi Biotec, San Diego, CA, USA) [1,10]. Some of the resting CD4+ T cells were cryopreserved immediately, using liquid nitrogen, as an uncultured control; the remaining cells were clonally expanded using a previously published protocol [10] and divided into equal portions for VOA and mouse engraftment, respectively. Cells engrafted in mice were grouped based on the VOA results into VOA-positive and VOA-negative groups.

NSG mice

Six-week old female NSG mice were maintained in micro-isolator cages within BSL-2 animal rooms following the protocol approved by the Institutional Animal Care and Use Committee at the University of Nebraska-Lincoln. Cryopreserved cells corresponding to VOA-negative CD4+ T cells (P46N) with VOA-positive (P46P) and uncultured (P46U) controls were thawed at 37°C and washed once using culture medium containing 100 U/mL IL-2. Cell viability was checked using a Vi-Cell XR cell viability analyzer (Beckman Coulter, Indianapolis, IN, USA); cells were resuspended into 200 µL of culture medium and injected into a mouse via a tail vein. Plasma viral load (pVL) and peripheral blood CD4+ T cells were quantified using qRT-PCR and flow cytometry, respectively, every 2 weeks.

Plasma viral load quantification

Viral RNA was extracted from plasma using QIAamp Viral RNA Mini kit (Qiagen, Valencia, CA, USA). pVL was determined by qRT-PCR, wherein cDNA was synthesised using Superscript III Reverse Transcriptase, RNaseOUT and RNase H (Life Technologies, Grand Island, NY, USA) with the gene specific primer: 5'- TTGCTACATCTCCTCTAT GCCAGAAGAAG-3', R1 5'-GTCCTGAGATCTGCTCCCACCC-3', F2 5'-ATGATACAGAATCTTGGAGAG-3', and R2 5'-GTTCTACCATGTCATTTACCTCACATTACAC-3'. The qPCR was run on C1000 Thermal Cycler and CFX96 Real-Time system (Bio-Rad) using TaqMan Fast Virus 1-Step Master Mix (Life Technologies, Grand Island, NY) with primers: forward 5'-GCCCTGATATATACTGTTCGGAGGAC-3', reverse 5'-GCAGGAGGACCTCAGAGA-3' and probe: 5'-/56-FAM/TTGCTACATCTCCTCTAT GCCAGAAGAAG-3' and probe: 5'-/56-FAM/TTGCTACATCTCCTCTAT GCCAGAAGAAG-3'. The detection limit of plasma HIV-1 RNA was 200 copies/mL and was determined through repeating endpoint detection from serial dilution of the AcroMetrix HIV-1 Panel (Life Technologies) [19].

Flow cytometry

Human CD4+ T cells isolated from mouse peripheral blood were measured using FACS Aria II flow cytometer (BD Biosciences, San Jose, CA, USA) after staining with antibodies against human CD45 (FITC conjugated; clone# HI30, BioLegend, San Diego, CA, USA), human CD3 (PE conjugated, clone# HIT3a, BioLegend), and human CD4 (Alexa Fluor 700 conjugated, clone# OKT4, BioLegend). Cells were blocked using Human TruStain FcX and Mouse TruStain fcX Antibodies (BioLegend) prior to staining. Raw data were analysed with FlowJo version 10.0 (FlowJo LLC, Ashland, OR, USA).

Sequencing of reactivated viruses

Viruses from the first pVL-positive samples were amplified using bulk RT-PCR and sequenced. The cDNAs were amplified using QS Hot Start High-Fidelity DNA Polymerase (New England Biolabs) with PCR primers: forward 5'-TAGAGCCCTGGAAGCTCAGCAAGAAG-3' and reverse 5'-TTGCTACTTTGTAGTCTCAGT-3'. The amplicons were confirmed by 1.0% agarose gel stained with ethidium bromide and bands were cut and purified by GeneJET gel extraction kit (Thermo Scientific). The amplicons of the 3kb spanning env region were sequenced using Sanger's method at Sequetech (Mountain View, CA, USA) with eight overlapping primers based on primer walking: F1 5'-TATGACATCTTCTCTAT GCCAGAAGAAG-3', R1 5'-GTCCTGAGATCTGCTCCCACCC-3', F2 5'-AGTACAGAATCTTGGAGAG-3', F3 5'-AGTTCGTGACCTCACATTACAC-3', F4 5'-CGAGATAGCAGGACAATTT-3', F5 5'-GGTAATGGGTTGCTCTGGAAAACTCA-3', F6 5'-GAAAGTGAGTTGCAAG-3', and R2 5'-GTTCTACCATGTCATTTACCTCACATTACAC-3'. The sequencing results were manually examined by peak and the ends of sequences containing ambiguous nucleotides were trimmed. The sequences were confirmed by overlapping identical regions. Then the sequences were assembled individually to obtain the 3-kb partial genome using Sequencher 5.0 (Gene Codes Corporation Ann Arbor, MI, USA). A phylogenetic tree containing the assembled virus sequences and a HXB-2 homolog region reference sequence was generated using MUSCLE 3.8 [20] and PHYML 3.0 [21] through the maximum likelihood method and displayed with FigTree 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/).

HIV-1 sequences obtained from this study have been deposited into GenBank under accession number KT223503, KT223504 and KT223505.

Results

Xenograft of human CD4+ T cells into NSG mice reactivated the proviruses from VOA-positive and VOA-negative samples

First, we wanted to test whether NSG mice engrafted with VOA-negative CD4+ T cells could reactivate proviruses. To compare in vivo NSG mouse reactivation of provirus with VOA, CD4+ T cells were first expanded in vitro and split into two equal portions before VOA. One portion was immediately cryopreserved for NSG mouse engraftment and the other portion was used for VOA serving as a surrogate for reactivation of the corresponding cryopreserved cells (Figure 1). After 3 weeks of VOA culture, HIV-1 p24 in the supernatant of each well was quantified using ELISA. The cryopreserved cells corresponding to the VOA-positive and the VOA-negative samples and uncultured positive control were injected into NSG mice via the tail vein. Plasma vRNA was quantified using qRT-PCR every other week.

Plasma viral RNA load was detectable at 4 wpi in both the VOA-positive (P46P, Figure 2A) and the uncultured sample (P46U, data not shown) as positive control. The pVL was undetectable at 2 wpi, became positive at 4 wpi (6.06 × 10⁵ copies/mL), and then remained at a plateau until the animal was euthanised at 14 wpi. In contrast, the pVL in the P46N engrafted mouse was undetectable before and at 8 wpi, became positive at 10 wpi (4.78 × 10⁶ copies/mL) (Figure 2B), and remained at a plateau until the animal was euthanised at 14 wpi.

Human CD4+ T cells engrafted in NSG mice can proliferate and support stable viraemia for a long time

We then checked whether immune-compromised NSG mice can maintain engrafted human CD4+ T cells for a long term using flow cytometry. As shown in Figure 2, we found that engrafted CD4+ T cells proliferated considerably in vivo starting from 2 wpi and peaked before the provirus was reactivated (4 wpi for P46P and P46U, and 10 wpi for P46N). Upon provirus reactivation, CD4+ T cells significantly

References

of note, active proliferation of CD4+ T cells (4 and 6 wpi) in the VOA-negative sample was several weeks ahead of pVL detection (Figure 3B). This temporal difference between CD4+ T cell proliferation and provirus reactivation indicates cell proliferation alone is not sufficient to reactivate provirus, and cell proliferation and provirus reactivation are independent events.

Reactivated proviruses from VOA-positive and VOA-negative CD4+ T cells were heterogeneous

To determine whether the reactivated proviruses from VOA-positive and VOA-negative CD4+ T cells were identical, a 3-kb HIV-1 partial genome spanning the full-length env from the first viraemic plasma samples was amplified using qRT-PCR and sequenced using Sanger’s method. The sequences of each sample are homogeneous with a pure single peak for every position. However, for different samples, the reactivated HIV-1 proviruses were heterogeneous (Figure 4A) and contained different in-frame insertions compared to the reference HXB2 sequence (Figure 4B).

Discussion

Curing HIV-1 infection by eradicating virus latency is one of the highest public health priorities. Enhanced co-culture assays, including VOA, have greatly deepened our understanding of HIV-1 latency; however, VOA can only reactivate a small fraction of intact proviruses. Thus, the underlying mechanisms of HIV-1 latency are not completely understood.

This study for the first time shows that engraftment of VOA-negative CD4+ T cells into NSG mice can reactivate proviruses. The results herein also demonstrate that HIV-1 latently infected CD4+ T cells engrafted into NSG mice can proliferate and survive for up to 14 weeks, which provides a prolonged window of opportunity to study HIV-1 latency and its reactivation. While VOA-positive CD4+ T cells and uncultured cells engrafted into NSG mice reactivated latent HIV-1 at 4 wpi, VOA-negative CD4+ T cells reactivated latent HIV-1 at 10 wpi. This delayed reactivation may mirror the delayed HIV-1 rebound after cessation of ART in HIV-1 functional controllers mediated through early initiation of ART in the ‘Mississippi child’ [22] and the ANRS VISCONTI study [23], as well as in the ‘Boston patients’ mediated through allogenic bone marrow stem cell transplant [24]. The delayed reactivation observed in the VOA-negative CD4+ T cells in this study supports the notion of heterogeneity of latently infected HIV-1 in resting CD4+ T cells [25,26]. The distinct sequences of reactivated proviruses from VOA-positive and VOA-negative CD4+ T cells indicate that there are different intact proviruses in resting CD4+ T cells with different reactivation efficiency.

Our study has demonstrated that provirus from engrafted human VOA-negative CD4+ T cells can be reactivated. A plausible explanation is that engrafted human CD4+ T cells underwent proliferation and expansion as shown in Figure 3, which might increase the quantity of provirus-bearing cells; meanwhile xeno-immune activation might also contribute to the reactivation of proviruses. However, the exact mechanism of provirus reactivation in this system remains to be studied. The temporal difference between the engrafted CD4+ T cell expansion and provirus reactivation indicates that cell proliferation does not directly reactivate provirus. Furthermore, the sequencing results revealed that the reactivated proviruses from VOA-negative and VOA-positive CD4+ T cells were different, indicating that latency reactivation regulation may be different.
We would like to point out the limitation of this case study. We operationally called cryopreserved cells corresponding to VOA-positive/negative cells; however, it is likely the split portions contained clonally expanded cells. Future studies that include more cases with determined clonality of engrafted cells by integration site sequencing analyses will be needed.

Collectively, this study clearly demonstrates that NSG mice can support long-term engraftment of human CD4+ T cells and reactivate proviruses from VOA-negative CD4+ T cells, which not only provide a large window for studying the HIV-1 latency at molecular and cellular detail, but can also be used to quantify the functional latent reservoir.

**Acknowledgements**

QL and ZY designed the experiments. ZY, GK and WL performed NSG mice experiments. ZY performed plasma viral load, flow cytometry and viral partial genome sequencing and data analysis. ZY and QL wrote the manuscript. The authors would like to thank Dr Robert Siliciano and Dr Ya-Chi Ho for providing patient samples and conducting viral outgrowth assay, and Lance Daharsh and Dr Fangrui Ma for their discussion and critical reading of this manuscript. This work was supported in part by NIH grant R01 AI111862 (to Li Q, Guo J), P30GM103509 and BEAT-HIV: Delaney Collaboratory to Cure HIV-1 Infection by Combination Immunotherapy 1UM1AI126620-01 (L Montaner, J Riley).
Figure 4. Sequencing results for reactivated HIV-1 from VOA-positive, VOA-negative and uncultured resting CD4+ T cells engrafted into NSG mice. (A) Phylogenetic relationship of reactivated HIV-1 from VOA-positive provirus, VOA-negative provirus, and uncultured resting CD4+ T cells using HXB2 as the reference sequence. (B) A representative region showing the differences between the reactivated viruses from VOA-positive, VOA-negative and uncultured sample contains different in-frame insertions as compared to the reference HXB2 sequence.

Competing interests
The authors declare that there is no conflict of interest in this study.

References